

Sequence Alignment

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 14:04:54 ; Search time 1 Seconds
(without alignments)
6.964 Million cell updates/sec

Title: us-09-944-896-49
Perfect score: 1876
Sequence: 1 ctctttgtccaccagccca.....tcagtgaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1856 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : seq264-1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764.5	94.1	1856	1	us-09-790-264-1
2	25.8	1.4	1856	1	us-09-790-264-1

ALIGNMENTS

RESULT 1					
us-09-790-264-1					
Query Match 94.1%; Score 1764.5; DB 1; Length 1856;					
Best Local Similarity 98.0%; Pred. No. 0;					
Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;					
QY	46	GCTCCATCCAGCTGAGAACACAGCGGGTGGCTGAGCCAGGCTGTGCAGGAGCACCTG	105		
DB	18	GCTCCATCCAGCTGAGAACACAGCGGGTGGCTGAGCCAGGCTGTGCAGGAGTGGCTG	77		
QY	106	ACGGGCCCCAACAGACCCATGCTGCATCCAGAGACCTCCCTGCGCGGGGGGATCTCTGG	165		
DB	78	ACGGGCCCCAACAGACCCATGCTGCATCCAGAGACCTCCCTGCGCGGGGGGATCTCTGG	137		
QY	166	CTGTGCTCTGCTGCTTGGCCACACCTGGGAGAGGTGTGGCCACCCAGCTGCAGG	225		
DB	138	CTGTGCTCTGCTGCTTGGCCACCCCTGGGAGAGGTGTGGCCACCCAGCTGCAGG	197		
QY	226	ACCAGGCTCCGATGGCGGAGCCCTGAACAGGAAGGAGATTTCTTGTCTCTCCCTGC	285		
DB	198	ACCAGGCTCCGATGGCGGAGCCCTGAACAGGAAGGAGATTTCTTGTCTCTCCCTGC	257		
QY	286	ACAACCGCTGCGAGCTGGTCCAGCCCTCGGCTGCATCGGAGGCTGGACTGGA	345		
DB	258	ACAACCGCTGCGAGCTGGTCCAGCCCTCGGCTGCATCGGAGGCTGGACTGGA	317		

QY	346	GTGACAGCTTGCCCAACTGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGA	405		
DB	318	GTGACAGCTTGCCCAACTGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGA	377		
QY	406	GCTGGCATCCGGCCTGTGGCGCACCTCTCAAGTGGGTGAACATGACGTGCTGCCCG	465		
DB	378	GCTGGCATCCGGCCTGTGGCGCACCTCTCAAGTGGGTGAACATGACGTGCTGCCCG	437		
QY	466	CGGGCTTGGCTCTTGTGAAGTGTGCTAGCTTATGTTGACAGGGGAGCGGTGCTA	525		
DB	438	CGGGCTTGGCTCTTGTGAAGTGTGCTAGCTTATGTTGACAGGGGAGCGGTGCTA	497		
QY	526	GCCACCGGCGAGGAGTGTGCTGCAAGCCACCTGCACCCACTACACGAGCTGCTGT	585		
DB	498	GCCACCGGCGAGGAGTGTGCTGCAAGCCACCTGCACCCACTACACGAGCTGCTGT	557		
QY	586	GGGCCACCTCAAGCCAGCTGGGTGTGGCGGACCTGTGCTGACGCCACAGACGGA	645		
DB	558	GGGCCACCTCAAGCCAGCTGGGTGTGGCGGACCTGTGCTGACGCCACAGACGGA	617		
QY	646	TAGAAGCTTGTGCTGCTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAAGCAA	705		
DB	618	TAGAAGCTTGTGCTGCTACTTCCCGGAGGCAACTGGGAGGTCAACGGGAAGCAA	677		
QY	706	TCATCCCTTATAAGAAAGGTGCTGTGCTGCTGCACAGCCAGTGTCTCAGGCTGT	765		
DB	678	TCATCCCTTATAAGAAAGGTGCTGTGCTGCTGCACAGCCAGTGTCTCAGGCTGT	737		
QY	766	TCAAAGCTTGGACCATGAGGGGGCTGTGAGGTCCCGAGAAATCTTGTGCATGA	825		
DB	738	TCAAAGCTTGGACCATGAGGGGGCTGTGAGGTCCCGAGAAATCTTGTGCATGA	797		
QY	826	GCTGCCAGAACCATGAGAGCTCAACATCAGCACTGCCACTGCTCCCTGCTGCT	885		
DB	798	GCTGCCAGAACCATGAGAGCTCAACATCAGCACTGCCACTGCTCCCTGCTGCT	857		
QY	886	ACACGGGCGAGATGCTCCAAAGTGCAGGTGCAGCTGCAGTGTGCAGGGCGGCTG	945		
DB	858	ACACGGGCGAGATGCTCCAAAGTGCAGGTGCAGTGTGCAGGGCGGCTG	917		
QY	946	AGGAGGAGTGTGCTGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAG	1005		
DB	918	AGGAGGAGTGTGCTGCTGTGACATCGGCTACGGGGGAGCCAGTGTGCCACCAAG	977		
QY	1006	TGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTCATGTG	1065		
DB	978	TGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTCATGTG	1037		
QY	1066	CAGAGGCGAGACCTTATACAGCCAGGATGAATGTTCAGAGAAAGCGGGTGTG	1125		
DB	1038	CAGAGGCGAGACCTTATACAGCCAGGATGAATGTTCAGAGAAAGCGGGTGTG	1097		
QY	1126	CCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGGCGGCTG	1185		
DB	1098	CCAGATCAAGAGCCAGAAAGTGCAGGACATCTCGCTTCTATCTGGGCGGCTG	1157		
QY	1186	CCACCAAGAGGTGACTGACAGTGTTCAGAGACCAAGAACTTCTGATCGGGCT	1245		
DB	1158	CCACCAAGAGGTGACTGACAGTGTTCAGAGACCAAGAACTTCTGATCGGGCT	1217		
QY	1246	ACAAGCCGCAAGGACTTCTCCGCTGGGCCACAGGGGAGACAGGCTTACCAAGT	1305		
DB	1218	ACAAGCCGCAAGGACTTCTCCGCTGGGCCACAGGGGAGACAGGCTTACCAAGT	1277		
QY	1306	TTGCTTTGGCAGCTGACACCAACGAGGCTGGTGTGGCTGAGTGTGCTGCTGG	1365		
DB	1278	TTGCTTTGGCAGCTGACACCAACGAGGCTGGTGTGGCTGAGTGTGCTGCTGG	1310		
QY	1366	GCAACTGCTGGAGCTGCAGGCTTCAGCTTCCTTCAACTGGACACAGGCTGCAAAA	1425		
DB	1311	GCAACTGCTGGAGCTGCAGGCTTCAGCTTCCTTCAACTGGACACAGGCTGCAAAA	1370		

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QY 1426 CCCGAACCGTTACATCTCCAGTTTCCAGGAGCACATCTCCGCTGGGGCCAGGGT 1485
Db 1371 CCCGAACCGTTACATCTCCAGTTTCCAGGAGCACATCTCCGCTGGGGCCAGGGT 1430
QY 1486 CCTGAGGCTGACACATGGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTG 1545
Db 1431 CCTGAGGCTGACACATGGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTG 1490
QY 1546 TCTGCCACCTGCTGTGGAAACAGGGCCAGGTTAAGACCAATGCTCATGTCCAAAGAGG 1605
Db 1491 TCCGCCACCTGCTGTGGAAACAGGGCCAGGTTAAGACCAATGCTCATGTCCAAAGAGG 1550
QY 1606 TCTCAGACCTTGCACAAATGCCAGAACTTGGGCAGAGAGAGGAGGAGGAGGAGGAGG 1665
Db 1551 TCTCAGACCTTGCACAAATGCCAGAACTTGGGCAGAGAGAGGAGGAGGAGGAGGAGG 1610
QY 1666 CAGGAGTGAGTGTAGAAAGAGCTGGGGCCCTTCGCTGCTTTTGGTGGAAAGATGGG 1725
Db 1611 CAGGAGTGAGTGTAGAAAGAGCTGGGGCCCTTCGCTGCTTTTGGTGGAAAGATGGG 1670
QY 1726 CTTCAATTAGATGGGAAAGAGAGAGACCCGCGAGTGGTCCAAAAGGCTCTCTCTTCC 1785
Db 1671 CTTCAATTAGATGGGAAAGAGAGAGACCCGCGAGTGGTCCAAAAGGCTCTCTCTTCC 1730
QY 1786 ACCTGGCCAGACCTGTGGGGAGGAGGAGCTTCCCTGTGGCATGAACCCACGGGGTAT 1845
Db 1731 ACCTGGCCAGACCTGTGGGGAGGAGGAGCTTCCCTGTGGCATGAACCCACGGGGTAT 1790
QY 1846 TAAATTATCAATCAGCTGAAAAA 1876
Db 1791 TAAATTATCAATCAGCTGAAAAA 1821
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RESULT 2

us-03-790-264-1/C

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Query Match 1.4%; Score 25.8; DB 1; Length 1856;
Best Local Similarity 67.9%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1124 GCGCCAGATCAAGAGCCAGAACTGGCAGGACATCCTCGCCCTTCTATCTGGGCC 1176
Db 1148 GCGCCAGATGAGAGGCGGAGATGCTGCACTTCTGGCTCTTGATCTGGGCC 1096
```

Search completed: September 17, 2003, 14:04:57
Job time : 2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2003, 14:00:33 ; Search time 0.001 Seconds
(without alignments)
202.930 Million cell updates/sec

Title: us-09-944-896-50

Perfect score: 2529

Sequence: 1 MLHPETSPGRGHLAVLLAL.....RNRYYICQFAQEHISRWPGS 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 446 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : seq264-2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	2447.5	96.8	446	1	us-09-790-264-2

ALIGNMENTS

RESULT 1
us-09-790-264-2

Query Match		96.8%;	Score 2447.5;	DB 1;	Length 446;
Best Local Similarity		97.1%;	Pred. No. 0;		
Matches 442;		Conservative 1;	Mismatches 3;	Indels 9;	Gaps 1;
QY	1	MLHPETSPGRGHLAVLLAL	1	MLHPETSPGRGHLAVLLAL	1
Db	1	MLHPETSPGRGHLAVLLAL	1	MLHPETSPGRGHLAVLLAL	1
QY	61	WVQPPADMRRLDWSLSLAQ	1	WVQPPADMRRLDWSLSLAQ	1
Db	61	WVQPPADMRRLDWSLSLAQ	1	WVQPPADMRRLDWSLSLAQ	1
QY	121	VEVYSLWFAGQRYSHAAG	1	VEVYSLWFAGQRYSHAAG	1
Db	121	VEVYSLWFAGQRYSHAAG	1	VEVYSLWFAGQRYSHAAG	1
QY	181	AYSPGGNWEYNGKTIIPY	1	AYSPGGNWEYNGKTIIPY	1
Db	181	AYSPGGNWEYNGKTIIPY	1	AYSPGGNWEYNGKTIIPY	1
QY	241	RLNISTCHCHCPPGYTG	1	RLNISTCHCHCPPGYTG	1
Db	241	RLNISTCHCHCPPGYTG	1	RLNISTCHCHCPPGYTG	1

301 TCCLRIDGDCFMVSSEADTYRARMKCKGVLAKIQAQKQVQDILAFYLGRLTNEVI 360
|||||
301 TCCLRIDGDCFMVSSEADTYRARMKCKGVLAKIQAQKQVQDILAFYLGRLTNEVI 360
|||||
361 DSDPETFNFWIGLTYKTAQDSFRWATGEHQAFQSPQPDNDHGLVWLSAAMGFGNCVEL 420
|||||
361 DSDPETFNFWIGLTYKTAQDSFRWATGEHQAFQSPQPDNDHGLVWLSAAMGFGNCVEL 420
|||||
421 QASAAFNWNDQRCCKTRNRYICQFAQEHISRWPGS 455
|||||
412 QASAAFNWNNQRCCKTRNRYICQFAQEHISRWPGS 446
|||||

Search completed: September 17, 2003, 14:00:33
Job time : 0.001 secs

